

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,096A
Source: IFW/6
Date Processed by STIC: 3/3/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

*Per 1.824 of Sequence Rules,
submit only one file in
computer readable form.*



IFW16

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/09/720,096A

TIME: 10:34:36

Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

2 <110> APPLICANT: Dan Nilsson
3 Thomas Janzen
W--> 4 <120> TITLE OF INVENTION: Method of preventing bacteriophage
W--> 5 infection of bacterial cultures
7 <130> FILE REFERENCE: 21134 PC 1
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/720,096A
C--> 8 <141> CURRENT FILING DATE: 2001-01-02
8 <150> PRIOR APPLICATION NUMBER: PA 1998 00878
9 <151> PRIOR FILING DATE: 1998-07-03
10 <150> PRIOR APPLICATION NUMBER: US 60/091,735
11 <151> PRIOR FILING DATE: 1998-07-06
E--> 12 <160> NUMBER OF SEQ ID: 6 (see p.4)
13 <170> SOFTWARE: FastSEQ For Windows Version 3.0

*Suggestion!
Consult
Sequence
Rules
for valid
format.*

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
16 <211> LENGTH: 32
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence
W--> 19 <220> FEATURE:
20 <223> OTHER INFORMATION: PCR-primer for the construction of plasmid with
21 deletion in thyA from strain CHCC373
W--> 22 <400> SEQUENCE: 1
E--> 23 tataatctgc agggtcacac tatcagtaat tg

**Does Not Comply
Corrected Diskette Needed**

*32 ← insert cumulative
base total at
right margin of each
line*

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<211> 4815

<212> DNA

<213> Lactococcus lactis subsp. cremoris

~~<213> STRAIN: MG1363~~ *this goes on <2237> line*

<400> 7

TATCTCGCTA AGTTAGGAGA ATAAG ATG ACA AAA GTA AAT TCA CAA AAA TAG
Met Thr Lys Val Asn Ser Gln Lys Tyr

do NOT show 2 <2137> line,
per sequence rules.

→ <2207> insert

<2237> ← put
52 response
on this
line.

show lower-case letters
for nucleotides

show any explanatory
information in the
<2207>-<2237>
section.

insert <2207> first.
It is a "header"
and never for a
response. Then,
insert <2237> and
put "STRAIN:MG1363"
on that line

use lower-case letters
for nucleotides

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<210> 8
<211> 2207
<212> DNA
<213> Lactococcus lactis subsp. lactis
<400> 8

TGA TTC TAC TTA CAT TCA CGT CTT TTG GAA CGT GCT GCC AAA TTA TCT
Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser
470 5 475 10 480 15

48

Per 1.822 of sequence rules, number
the amino acids (in a mature protein)
beginning with "1," even if they're in a coding
sequence.

Please follow above example in re-numbering
amino acids. Same error in sequences 9,
10, and 11.

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<210> 11 last sequence is submitted file
<211> 375
<212> DNA
<213> Trichoderma reesei
<400> 11

TACTCGAAGA ATTCCGGCAG AGGCTGATTG CTCTCGGTCA TCTGCCAAG ATG TTC

Met Phe
260

55

use lower-case letters

and →
re-do numbering

VERIFICATION SUMMARY

DATE: 03/03/2006

PATENT APPLICATION: US/09/720,096A

TIME: 10:34:37

Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
 L:8 M:270 C: Current Application Number differs, Replaced Current Application No
 L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:12 M:283 W: Missing Blank Line separator, <160> field identifier
 L:19 M:283 W: Missing Blank Line separator, <220> field identifier
 L:22 M:283 W: Missing Blank Line separator, <400> field identifier
 L:23 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:1
 L:29 M:283 W: Missing Blank Line separator, <220> field identifier
 L:32 M:283 W: Missing Blank Line separator, <400> field identifier
 L:39 M:283 W: Missing Blank Line separator, <220> field identifier
 L:42 M:283 W: Missing Blank Line separator, <400> field identifier
 L:49 M:283 W: Missing Blank Line separator, <220> field identifier
 L:52 M:283 W: Missing Blank Line separator, <400> field identifier
 L:59 M:283 W: Missing Blank Line separator, <220> field identifier
 L:63 M:283 W: Missing Blank Line separator, <400> field identifier
 L:70 M:283 W: Missing Blank Line separator, <220> field identifier
 L:74 M:283 W: Missing Blank Line separator, <400> field identifier
 L:82 M:280 W: Numeric Identifier already exists, Organism not replaced.
 L:83 M:283 W: Missing Blank Line separator, <400> field identifier
 L:84 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=7
 L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
 L:375 M:283 W: Missing Blank Line separator, <400> field identifier
 L:376 M:112 C: (48) String data converted to lower case,
 L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
 M:112 Repeated in SeqNo=8
 L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
 L:384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8

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VERIFICATION SUMMARY

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Input Set : E:\Sequence Listing\9810089_final.txt

Output Set: N:\CRF4\03032006\I720096A.raw

L:387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:405 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:417 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:475 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:8
L:517 M:283 W: Missing Blank Line separator, <400> field identifier
L:518 M:112 C: (48) String data converted to lower case,
L:520 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
M:112 Repeated in SeqNo=9
L:523 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:529 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:535 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:541 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:547 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:556 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:559 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:656 M:283 W: Missing Blank Line separator, <400> field identifier
L:657 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:714 M:283 W: Missing Blank Line separator, <400> field identifier
L:715 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (11)